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Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

1/61

FIGURE 1 (SHEET 1)

		:	
	1020	TTAAGATCTCCAGATCCTGGCATCCTGGCTTATAAGCCAGGCTCAG	961
		ENEHFRDKSELEDKKVEEGK	
	960	GAAAATGAACATTTCCGGGACAAATCAGAACTTGAAGATAAAAAGGTAGAAGAGGGGG	901
		,	
	900	TTTTTATCAAATCATATTAATTCATATTTCAAACGTAAGGAAAAAATGTCTCAACAAA	841
		K R S L F H Y T S S I T T K F G D S F Y	
	840	81 AAACGCAGTCTTTTTCATTACACAAGTTCTATAACCACAAAATTTGGAGACTCATTCTAC	781
		EKSPFPEEKSHIIDKEEDIG	
	780	21 GAAAAGAGTCCTTTTCCAGAAGAGAAAAGTCACATTATAGACAAAGAAGAAGATATAGGT	721
		K Q K N I K Q A I K S L K K Y S D K S A	
	720	VAACATCAAACAAGCCF	99
		LAQFKPSSQILRKVSDSGWL	
	660	01 TTAGCTCAATTTAAGCCAAGTTCCCAAATTTTAAGAAAAGTATCGGATAGTGGCTGGTTA	601
		STLNSVSKAVFGNQNEMISR	
	600	41 AGTACTTTGAACTCTGTTTCAAAGGCTGTTTTTGGCAATCAAAATGAAATGATTTCACGT	541
		LSTSAPKGLTKVNICMSRIK	
	540	81 CTTAGCACTTCTGCTCCCAAGGGACTTACAAAAGTGAACATTTGTATGTCCCCGTATTAAA	481
		S C S K H C Y S P S N H G L H I G I L K	
	480	TCTI	421
•		LQRGFHINIIRCKWIKSEAH	
	420	CTACAAAGAGGTTTTCATACA	361
		SKQLYFLFSPKHYWRISHIS	
	360	01 AGCAAGCAACTGTATTTCTTGTTCTCACCTAAGCATTACTGGAGGATAAGCCACATCAGT	301
		TVDIYIYLLSNARSVCGKQR	
	300	ACTGTAGATATATATTTACCTCCTTAGTAATGCAAGAAGTGTTTGT	241
		SEQ ID NO: 1 M S I N L	
	240	81 TCAAGAAGTGAGAGAATGTCATAGAAAATAAATGATTTTAAGTTATGTCTATTAATCTG	181
	180		121
-	120	61 GCCGCTGCAGCCCTAGTGACTGCGGCCTGCATCCCGATTGTCTTCTTCCTCCAAGGTCTAC	9
	C	${ t TGGAAGCTCAGCTGATGCAGGCCGGTTGGAGTGGACGTCATTGCCGGGAACGAGCGAG$	널
	,		EQ

Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

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THEREFOR Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

3/61

FIGURE 1 (SHEET 3)

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Q

1981	TTTCCTGGAATCAACTCTCATTATTTGGGAGGCTGTCAGTATAAAATGTGGCAGGCCATT	2040
2041	TTGGGAAATGATCTTCAT	2100
2101	3CATGAGTGTAAATGT	2160
	Q D G G L L L N N P S A L A M H E C K C	
2161	CTTTGGCCAGATGTGCCGTTAGAGTGCATAGTATCCCTGGGCACTGGACGTTATGAGAGT :	2220
,2221	GATGTGAGAAACACGGTAACATACACAAGCTTGAAAACTAAACTTTCTAATGTTATCAAC:	2280
•		
2281	STTACCTCCTGACACC	2340
2341	TCGAAATGAA	2400
	YFRFNPVMCENIPLDESRNE	
2401	CTGGATCAGCTGCAGTTGGAAGGGTTGAAATACATAGAAAGAA	2460
	K L D Q L Q L E G L K Y I E R N E Q K M	
2461	IGATTGG	2520
	K K V A K I L S Q E K T T L Q K I N D W	
2521	TTTTCAAAATTGTGATGAGTA	2580
	IKLKIDMYEGLPFF <u>SK</u> L-	
2581	TCAACCACATTCAATAAGGAA	2640
2641	TIGTGGGGTTCGACATGAGTTAACTTTGAAATACGTATGAATTCTGGAGAATCCTGAAAA ;	2700
2701		2760
2761		2820
2821		2880
2881	TGCCGAACAAGAAACCGAAAGCTATATTGTACTGTGTATTTTTACTTTAGTCCTCATAAT 2	2940
2941		3000
3001		3060

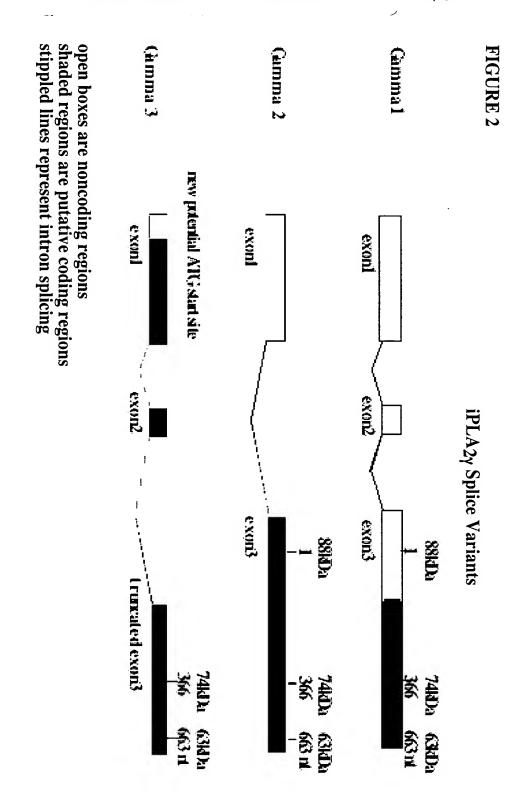
Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

>	SACTIMATE CATTITIAAAATTTAATTTTTGTTCATAATGTAGCTCCCCTTTAACCTTTACCCTTTAAAATTTTTTTT	3361 BOCOTA TOTO TOTO TOTO	3301 TACTGAGGAGATATTCCTATCATTAACAAAAATAACTTATTAACAAAAATAAACTTATTA	300 300 TELLARCITTICCAGATCTAACACTAGCTTATTCTTCCCTGTTATAAAATGGTTTGAACT		3180 TTAAAAAAGGTGAAGTTCCAGTCAACCACACACACACACA	3121 ACAIAAAAAAGAACCAGATACAGTTTTCTATTCAGATATGTTTATTTA	3120 STRITTERCATTING 3120
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THEREFOR
Inventor: Richard W. Gross et al.
Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070



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Gordon F. Sieckmann, Phone 314-621-5070

6/61

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Fig 3 Splice Variants of iPLA27

Title: CALCIUM INDEPENDENT PHOSPHOLIPASE $A_2\gamma$ THEREFOR

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

7/61

FIGURE 4 (SHEET 1) Full-length iPLA27

Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3' Sense primer M444 Primers for PCR amplification of full-length 88kDa iPLA27 5'-TTTTGTCGACATGTCTATTAATCTGACTGTAGATA-3'

Sequence of 88kDa iPLA27:

SEQ ID NO:13 atgtctattaatctgactgtagatatatatttacctccttagtaatgcaagaagtgtt SEQ ID NO:1 3 ataagccacatcagtctacaaagaggttttcatacaaacataataagatgtaaatggacc tgtgggaagcagaggaagcaagcaactgtatttcttgttctcacctaagcattactggagg aaaagtgaagcacattct gaaatgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcg atgtcccgtattaaaagtactttgaactctgtttcaaaggctgtttttggcaatcaaaat attgggattttgaaacttagcacttctgctcccaagggacttacaaaagtgaacatttgt gatagtggctggttaaaacagaaaaacatcaaacaagccatcaaatctctgaaaaaatat ggagactcattctacttttatcaaatcatattaattcatattcatattcaaacgtaaggaaaaa gaagaagatataggtaaacgcagtctttttcattacacaagttctataaccacaaaattt agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa ۲j ഗ Q ഗ ഗ Ø Н 二 ഥ U Z Н ۲ O × ㅈ 耳 ഗ ۲ × ഗ ㄷ Ľ ۲ ഗ ᄪ 涔 H 껔 >tgcagtaagcactgttactctccaagcaaccatggtttacat Ω н ល Ю O × Z Ø O ۲ н ល Ø ຜ ល വ × ᄖ Q 꺽 × z ល ۲ ש 二 ഗ I × D ᄖ Н 괴 μj שי ⋖ a H 띡 ש × I ש ٢ К н ഗ ഗ × К ᄪ Ю U × ល z വ Þ 団 ス Н ល ש $^{\times}$ H Ю К လ ഗ Н Ы 4 വ Н н ເນ 뾔 ഗ ㅈ × z Ħ × 二 ഗ ۲ ᄖ H a I Н H Q Ħ z Q × К z >ス Н н Σ × ۲ Ю z വ Ø ഗ

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Inventor: Richard W. Gross et al.
Docket No.: 15060-42
Gordon F. Sieckmann, Phone 314-621-5070

8/61

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Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

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Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

10/61

FIGURE 5 (SHEET 1)

Sequence of 77kDa iPLA₂y;
starting at amino acid 101 (nucleotide 301)
Primers for PCR amplification of full-leng
Sense primer M534 5'-TGAACGTCGACA

Sense primer M534 Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3' Primers for PCR amplification of full-length 88kDa iPLA2? NO:16 5'-TGAACGTCGACATGTCCCGTATTAAAA-3 н ۲ വ ⋖

SEQ ID NO: 14 SEQ ID NO: 12

gaatetgtaeataeggtggaeaageetaeaagteettetgegataeetgatgttetteaa gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca gatagtggctggttaaaacagaaaaacatcaaaccaagccatcaaatctctgaaaaaatat DSGWLKQKNIKQAIKSLKKY atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag gaagaagatataggtaaacgcagtctttttcattacacaagttctataaccacaaattt ggagactcattctacttttatcaaatcatattaattcatattcaatccaaacgtaaggaaaaa agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa gaaatgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcg .tcaactaaacaaagtattgctaactttcttctcgtcccacggaaggtgtacaagct 댐 U ល U × ļ.īļ Н ß н ດ К O Þ ល 团 ц × 回 г Ю ט × ᆫ z × × ं [म × ໝ ഗ ഗ ໙ O שי ы 二 z г Ы נגו U I Н 긔 ᄖ μj × ש ល Н 二 שי Ø ש К Ю טי z U ᄖ ល н × Ņ Ħ Þ ໝ ຜ К ഗ Ю ㅈ н 闰 ᄖ ഗ Ø н H × Н 耳 ۲ × н H Ħ Н שי U × Н * Н $\boldsymbol{\varkappa}$ Ħ × × × A К × × ļΤļ ×

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THEORE 5 (SHEET 2

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

12/61

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Title: CALCIUM INDEPENDENT PHOSPHOLIPASE A, Y THEREFOR

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

13/61

starting at amino acid 122 (nucleotide 364) Sequence of 74kDa iPLA, y:

Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3' Sense primer M533 Primers for PCR amplification of full-length 88kDa iPLA27 5'-TCAAGTCGACATGATTTCACGTTTAGC-3

ë No 18 ggagactcattctactttttatcaaatcatattaattcatatttcaatccaaacgtaagġaaaaa gatagtggctggttaaaacagaaaaacatcaaacaagccatcaaatctctgaaaaaatat tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca ttagtaggtggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca <u>atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag</u> gaagaagatataggtaaacgcagtctttttcattacacaagttctataaccacaaaattt agtgacaaatcagcagaaaagagtccttttccagaagagaaaagtcacattatagacaaa atgatttcacg Ħ tgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa Ø ᄪ U Q O × × Q К Н Ħ tttagctcaatttaagccaagttcccaaattttaagaaaagtatcg ۲ H Ħ щ × 떠 ス ۲ O z U Ø × Ю × တ ᄪ ഗ လ ഗ ıΊ z ש z ש 出 z ۲ שי щ 二 U μĵ × Ø H ם Ø Ю a ഗ Ч Q z К H ഗ D $\boldsymbol{\varkappa}$ Н (T) Ø ഗ Ø Ø ഗ Ľ K ഗ н ש × ᄖ щ ഗ К H × Н I æ H a įŦj × Н н × U × Н U × O G ス Ħ × Ю × × μj ល

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Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

14/61

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RIGORE 6 (SHEET 2

Inventor: Richard W. Gross et al.
Docket No.: 15060-42
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E N I P L
TGttgaaatacatagaaaga
K Y I E R
Pacaactctgr
T L

THEREFOR

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

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FIGURE 7 (SHEET 1)

Sequence of 63kDa iPLA_{$\gamma\gamma$}

Sense primer M530 Primers for PCR amplification of full-length 88kDa iPLA27 starting at amino acid 221 (nucleotide 661) 5'-GTAAGTCGACAATGTCTCAACAAAAGG-3

caggctgcagttagagaaattttggccctaattggctatgtggatccagtgaaagggaga actagggttgaagaactgacttttcatcttctagaatttcctgaaggaaaaggagtggct aacaggacccgggcattagttcaggcattaagaagaacaactgacccaaagctctgcatt gaggagaaaaagcgtttatctcttcagcgagaaaagattatcgcaagggtgagtattgat gtttcaactaaacaaagtattgctaactttctttctcgtcccacggaaggtgtacaagct gaatctgtacatacggtggacaagcctacaagtccttctgcgatacctgatgttcttcaa gtagaagaggggaaattaagatctccagatcctggcatcctggcttataagccaggctca atgtctcaacaaaaggaaaatgaacatttccgggacaaatcagaacttgaagataaaaag tcagaagaacaggaagagcctgctaaaactgatcaggctgtcagcaaagacagaaatgca Ħ ഗ Ħ ຜ ഠ വ 떠 ᄪ ggttatattggtggacttgtccccaaattaaagtatgattcaaagagtcag Ø Ø Н × [T] К O ᄪ Ħ שי tatttattacgactgagacaaattaaggatgaaactctt 耳 Ø × z 耳 שי H Ħ < H (F) U שי ۲ Ħ Ø \asymp × ល ש U н Н D ۲ Ø × ഗ Н ש ഗ a D К H D H שי × U 凹 г Ħ שי a ⋖ വ Ħ ഗ A ם æ ⋖ שי >۲ z O ഗ Þ U Ø

Reverse primer M458 5'-GCATAGCATGCTCACAATTTTGAAAAGAATGGAAGTCC-3' SEQ ID NO: 12 **SEQ ID NO: 20**

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

17/61

ttacctcctgacacctattttagattcaatcctgtaatgtgtgaaaacatacctctagat ggaaatgatcttcatcaagatggaggtttgcttctgaataacccttcggcattagctatg agaaactatggtcattttcctggaatcaactctcattatttgggaggctgtcagtataaa aaggtagctgctgtaagtaccatagtaaatagagggataacacccaaagcttt cttaaggataggatgggatctgcactgatgattgaaacagcaagaaaccccacatgtcct LKDRMGSALMIETARNPTCP ggaacagtaaaaatgagttggagccatgcatttatgacagtcaaacatgggaaaacatt Ħ Q Н tgtaaatgtetttggeeagatgtgeegttagagtgeatagtateeetgggeaet U 4 × Q I . ເນ ᆈ ល U שי н Σ × Q Н ഗ Q U Ω D Ø Н ⋖ H Н Н z z щ gctccaggctactt Ħ ഗ Ø 긔 Þ שי н г ۲ ດ 团 שי H К a r ப К н Q U Q I × Н ۲ 耳 Ω z К н ល Ø Н שי 긔 Q שי Ø ഗ tgcagaatatgcattg 3 Q ス Н ഗ Ю Ø Þ ഥ Q Σ Q Ю К 피 Ħ К 4 z gttc × ļΤļ U

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Inventor: Richard W. Gross et al. Docket No.: 15060-42

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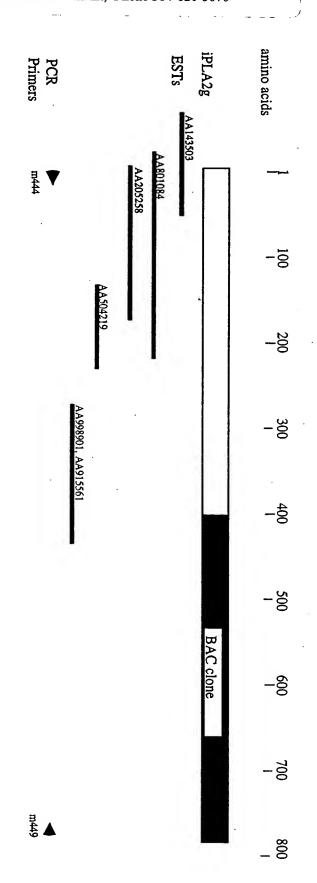
×	aaattgtga	×	aaa	z	aatgaac	Ħ	gaaagtcgaaatgaaaagctggatcagctgcagttggaagggttgaaatacatagaaaga	FIG		t	•
Ľ	ttg	н	att	Ħ	gaa	S S	agt	URE		ŀτ	j
•	tga	z	aat	Ю	caa	Ø	cga	FIGURE 7 (SHEET 3)		'n	נ
		U	gat	×	aaa	z	aat	HS)		t	,
		DWIKLKTDMYEGLP	tgg	Q K M K K V A K I L	atg	NEKLDQLQL	gaa	田田丁		-	3
		н	ata	×	aaa	*	aag	ω		н	4
	i	*	aaa	×	aaa	۲	gtg			12	1
		۲	tta	⋖	gtt	a	gat			7	J
		*	aaa	Þ	gca	Ø	cag			•7	1
		Н	act	×	aaa	Ľ	ctg			2	4
		ט	gat	н	ata	Ю	cag			•1	J
		3	atg	L	tta	۲	ttg			<	=
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		Ħ	gaa	Ø	caa	Q	999			(7
		Q	gga		gaa	۲	ttg			t	5
		۲	t t	۲	aaa	×	aaat			7	2
		ש	ccat	н	aca	К	caca			٠,	_
	•	μij	cta	H	act (Н	atag			h	C
		Ή	lattaatgattggataaaattaaaaactgatatgtatgaaggacttccattctttca	E K II II L	;aaaaaatgaaaaaagttgcaaaaatattaagtcaagaaaaaacaactctgcag	BULKKIE	gaa			77 77 77 77 77 77 77 77 77 77 77 77 77	-
		ഗ	Ca	Ю	cag	æ	эgа			t	=

Title: CALCIUM INDEPENDENT PHOSPHOLIPASE A₂γ POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS THEREFOR Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070





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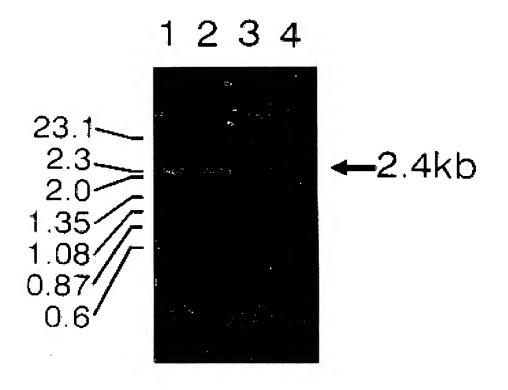


FIGURE 9

THEREFOR

GAA AAG GCA AGT TGT TCA GT gtgctt..tcgcaag

Q

Exon 6 GTG AGT

(Gross lab) JBC 275: 9937, 2000

Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

B.Potential Splice Variant (gt/ag)

21/61

Potential Alternative Exon 5 Splice Variant of Human iPLA27

A. Reported Splice Sequence (gc/ag)

Exon 5 (SEQ ID NOS 43-44)
CAG CGA GAA AAG
Q R E K

gcaagtt...ttgtag

ATT ATC GCA AGG GTG AGT

BBRC 272: 320, 2000 (Tanaka et al)

The incidence of gc/ag splice variants like the one shown in "A" is 0.56%. The variant "A" has been reported in the literature,

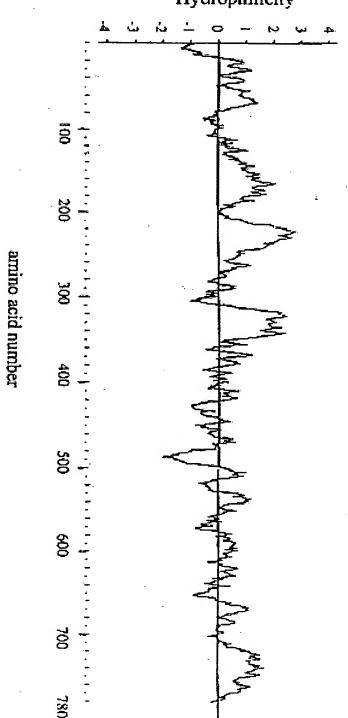
reported in GenBank, and cloned in our lab.

The splice variant gt/ag occurs with a frequence of 98.71% among genes. However, variant "B" iPLA27 sequence has not been cloned.

THEREFOR
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Docket No.: 15060-42
Gordon F. Sieckmann, Phone 314-621-5070

22/61

Hydrophilicity



TOUKE I

Inventor: Richard W. Gross et al. Docket No.: 15060-42

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23/61

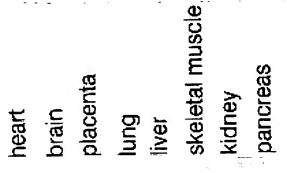




FIGURE 12

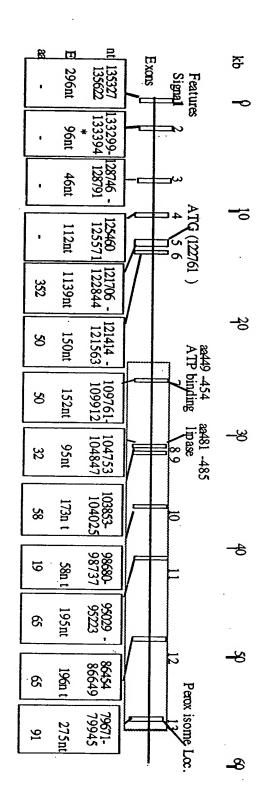
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24/61

FIGURE 13

*5 end has been also been reported as 133114 and 133464 in GenBank



Inventor: Richard W. Gross et al.
Docket No.: 15060-42
Gordon F. Sieckmann, Phone 314-621-5070

25/61

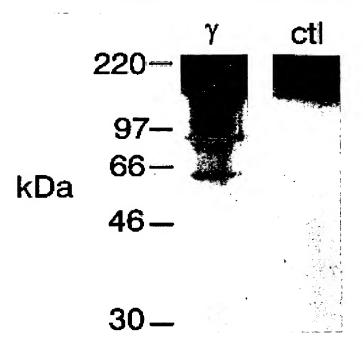
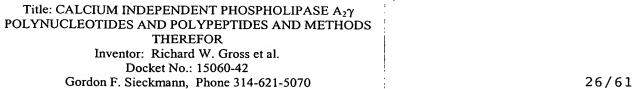


FIGURE 14



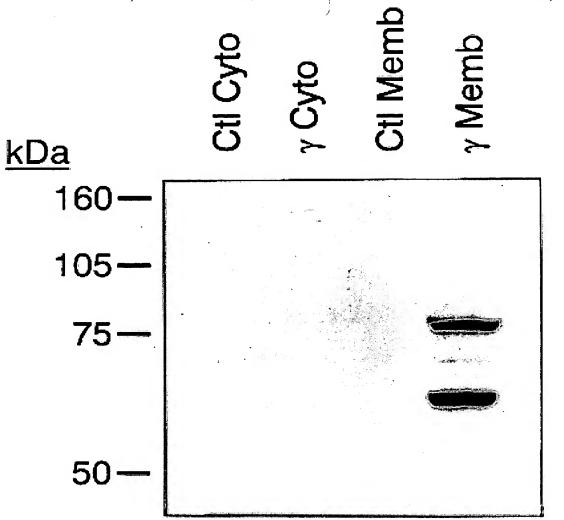


FIGURE 15

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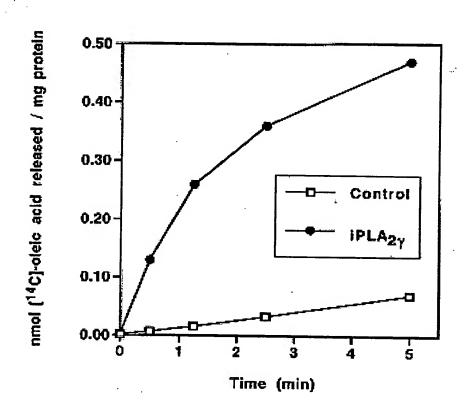


FIGURE 16

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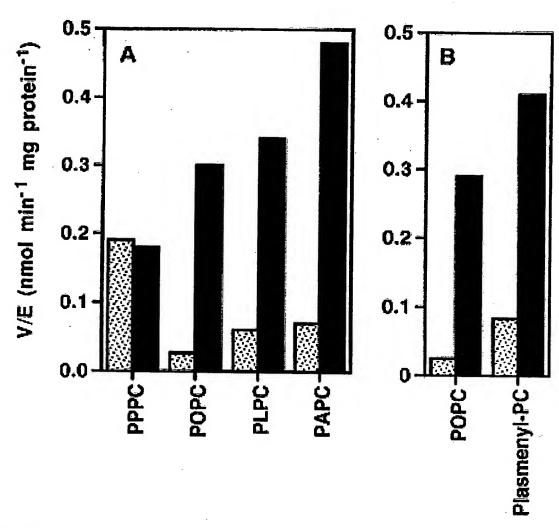


FIGURE 17

Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

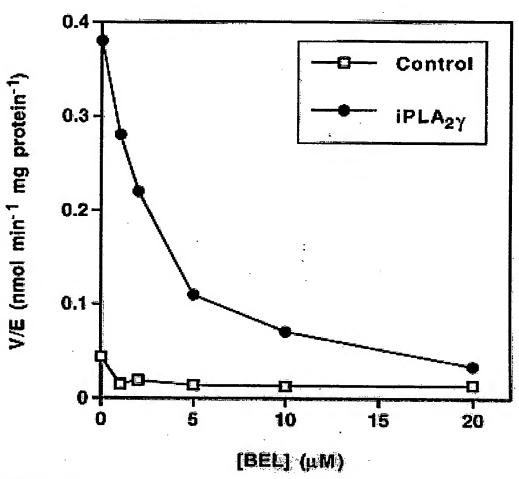
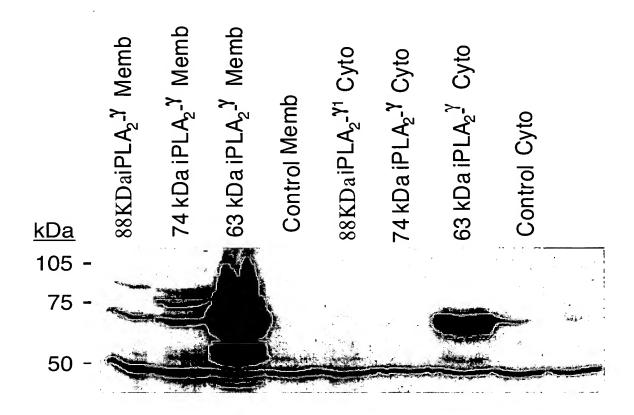


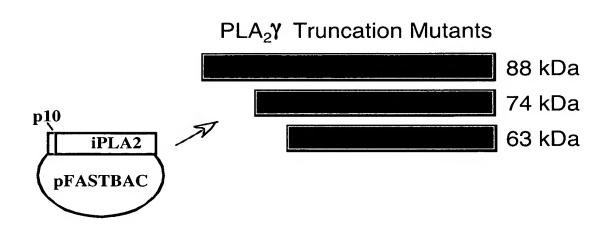
FIGURE 18

Inventor: Richard W. Gross et al. Docket No.: 15060-42

FIGURE 19

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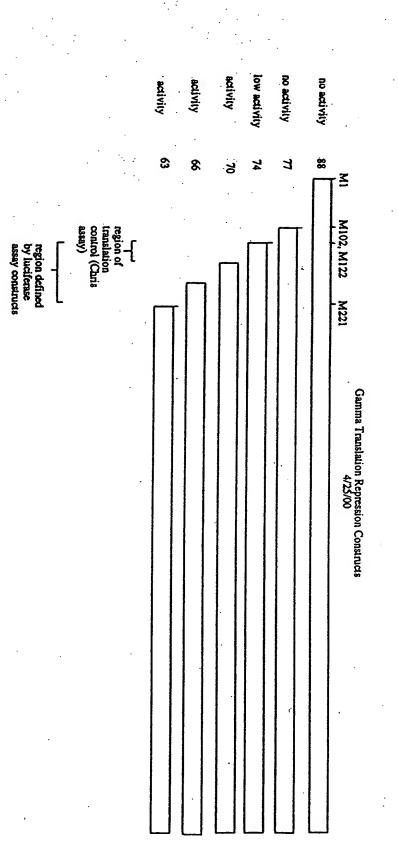




Title: CALCIUM INDEPENDENT PHOSPHOLIPASE A₂γ POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS

THEREFOR
Inventor: Richard W. Gross et al.
Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070



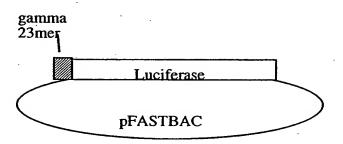
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Gordon F. Sieckmann, Phone 314-621-5070

32/61

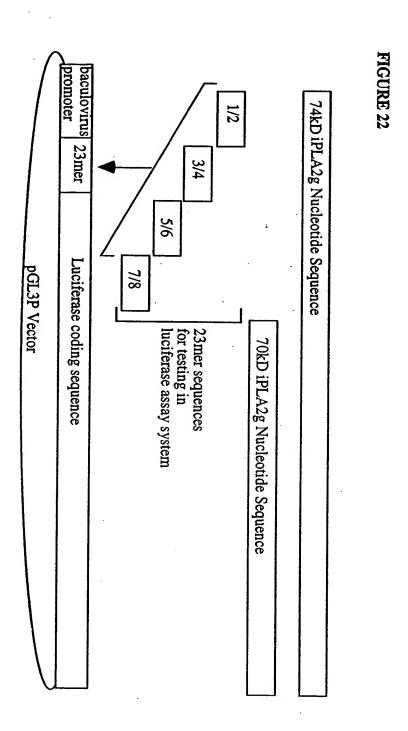
FIGURE 21

Additionally, iPLA27 sequences were inserted by ligation of 15-23mer annealed phosphorylated oligonucleotide pairs 5' of full-length luciferase coding sequence cloned into pFASTBAC via NotI/XbaI restrictions and then luciferase activity of recombinant protein produced in the Sf9 system was subsequently measured using the Luciferase Assay System of Promega.



THEREFOR
Inventor: Richard W. Gross et al.
Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070



Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

34/61

FIGURE 23. iPLA, 7 Repressor Region

SEQ Ses	oas Oas	OBS OBS	ðas ðas ðas	fo
SEQ ID NO: 35 SEQ ID NO: 39	###	SEQ ID NO: 33 SEQ ID NO: 37	SEQ ID NO: 10 SEQ ID NO: 32 SEQ TD NO: 36	d deo
NO: 35	ID NO: 34 ID NO: 38	NO: 33	ID NO: 10 ID NO: 32 ID NO: 36	nde Joq
ယ ယ ယ	ω ω 4 8	33	10 32	у1а ө <i>вв</i>
			tog	ted
	•	•	at acct gga	of Of
				igo ¡PI
			ettca ttca ttca	Phosphorylated oligo pairs for repression of $iPLA_{j}\gamma$ in
			ID NO: 10 atgatttcacgtttagctcaatttaag ID NO: 32 tcgacctgatttcacgtttagctcaatt ID NO: 36 ggactaaagtgcaaatcgagttaaccgg	Phosphorylated oligo pairs for repression of $\mathrm{iPLA}_{1}\gamma$ in the luciferase expression system:
			rato Ctag Ctag	tb
		i.	gagt ctca	ь Н
		tog	att att aac	1011
		tcgactaagccaagttcccaaattttaa gattcggttcaagggtttaaaatt	caag cgg	Eera
		otaagccaagttcccaaattttaa gattcggttcaagggtttaaaattccgg	CCaa	186
)Caa	igtt	<u>x</u>
		gttc	cca	pre
	_	icca:	laat:	188
	togacgaaaagtatoggat gottttcatagoota	aatt ttaa	t t ta	g
	logaaaagtatoggatagtggotgg gottttoatagootatoaoogaoooogg	tta	laga	вув
	aaag	t ccc	. aaac	tem
	ytat :ata	ğ	gtat	:
	300g		cgga	
	atag catc		atag	
	rtgg acc		1599	
togaat	tagtggctgg atcaccgacc		ctgc	
gacı	, , ,		jtta	
ttaa gtot	ш		ааас	
ttt:			;aga	
togacttaaaacagaaaaacatcaaa gaattttgtctttttgtagtttgtccgg			atgatttcacgtttagctcaatttaagccaagttcccaaattttaagaaaagtatcggatagtggctggttaaaacagaaaaacatcaaaca ctgatttcacgtttagctcaatt gactaaagtgcaaatcgagttaaccgg	
iget.			icat	
cato			Caas	
cgg cgg			Ca	

tcgacttaaaacagaaaaacatcaaaca

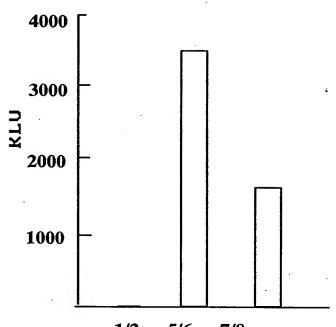
Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

35/61

FIGURE 24



1/2 5/6 7/8 iPLA2g 23mer Luciferase Constructs

Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

36/61

FIGURE 25

881	Da J				
mouse	MSINLTLDIYIYFLN	NARSLEGKORSKOLH	FVCE KOYWRMNHVN		
rat	MSINLTLDIYIYFLN	NARSFEGKORSKOLN	FLCS KOYWRMNHVN		
human	MSINLTVDIYIYILS	NARSVEGKORSKOLY	FLFSPKHYWRISHIS		
mouse	VHREFHTSKKSCKWN VHREFHTSKKSCKWN LORGFHTWIIRCKWT	RSEAH CSKHWHSPS	NHGLHFGIVRISTSA		
rat		RSEAH CSKHWHSSS	NHGVHIGIVKISTSA		
human		RSEAHSCSKHCYSPS	NHGLHIGILKISTSA		
mouse rat human	PKGLTKVSIHNSRIK PKGLTKVSIHNSRIK PKGLTKVNICNSRIK	741 STLNSVSKAT FGSON STLNSVSKAT FGSON STLNSVSKAVFGNON	Da ↓ EMVTRLAQFKPSSRI EMVSRLAQFKPSSRI EMISRLAQFKPSSQI		
mouse	LRKVSDKGWLKQKNV	KQAVESLKNYSDKSA	GKNSLAEOKSYFAIK		
rat	FRKVSDRGWLKHKNV	KQAIESLKNYSDKSA	EKNSFAEOKSYFAIK		
human	LRKVSDSGWLKQKNI	KQAIKSLKKYSDKSA	EKSPFPEEKSHIIIK		
mouse rat human	EEDSGKH\$LFHYTYG EEGSDKH\$LYHYAYR EEDIGKR\$LFHYTSS	ITTRFGESFSVLANH ITTRFGESFYFLANH ITTKFGDSFYFLSNH	63kDa INSYFKAKEKMSQTK INSYFKAKEKMSQCK INSYFKAKEKMSQCK		
mouse	EDKQLQDKPDIE	ERKSSEPGPDTVA	DRPDSESPLEVKUKU		
rat	EDRQLQDKPCLE	ESKSISPSPDILT	DRPDSGPPLNVEDKL		
human	ENEHFRDKSELEDKK	VEEGKLRSPDPGILA	YKPGSES VHTVDKP		
mouse	SSPTQMPEAHPVSAK	QSIANFLSRPTEGVQ	ALVGGYIGGLVPKLK		
rat	SSSTQLPEALPVSTK	QSIANFLSRPTEGVQ	ALVGGYIGGLVPKLK		
human	TSPSAIPDVLQVSTK	QSIANFLSRPTEGVQ	ALVGGYIGGLVPKLK		
mouse	SDPKSPPEEORVSAK	TEQAVBIDEKAEEKK	RVLLQDEKITARVST		
rat	SDPKSQPEEEBEPSK	TDEPICKDEKAEEKK	RVLLQREKITARVST		
human	YDSKSQSEEOREPAK	TDQAVSIDENAEEKK	RLSLQREKITARVST		
SEQ ID NO: 40 = N terminal 353 amino acids of mouse iPLA 2γ					

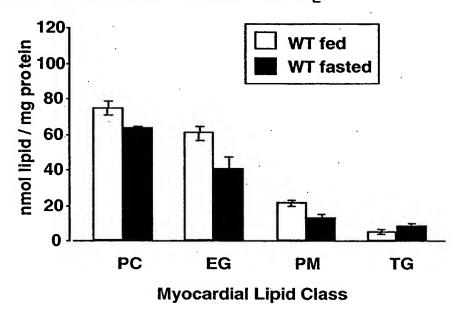
N terminal 353 amino acids of rat iPLA 2γ **SEQ ID NO: 41 =**

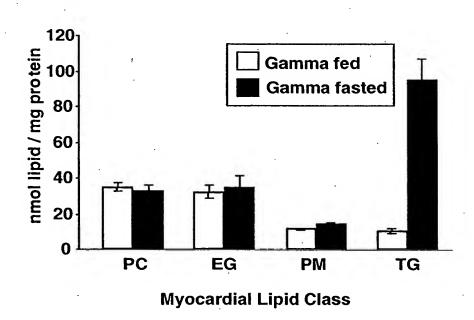
SEQ ID NO: 42 = N terminal 359 amino acids of human iPLA 2γ Inventor: Richard W. Gross et al. Docket No.: 15060-42

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37/61

Fig. 26 Myocardial TAG Content of Fasted WT vs iPLA27 Transgenic Mice





PC = Phosphatidylcholine

EG= Ethanolamine Glycerophospholipids

PM= PLasmalogen

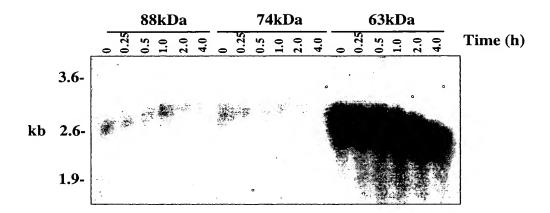
TG= Triacylglyceride

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38/61

FIGURE 27



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Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

39/61

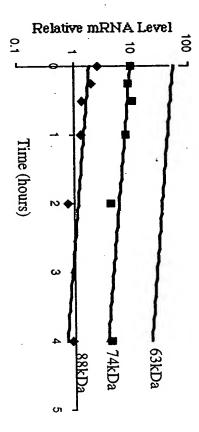


FIGURE 28. Quantitative PCR analysis of RNA stability of truncated iPLA2 γ Sf9 Expression

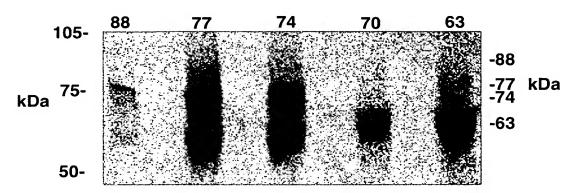
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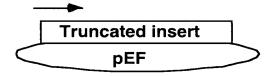
FIGURE 29

Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

40/61

Constructs





Inventor: Richard W. Gross et al.

Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

41/61

FIGURE 30

Aorta Liver Sf9

-74kD

== -63kD

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iPLA₂ Gamma Functional Domains

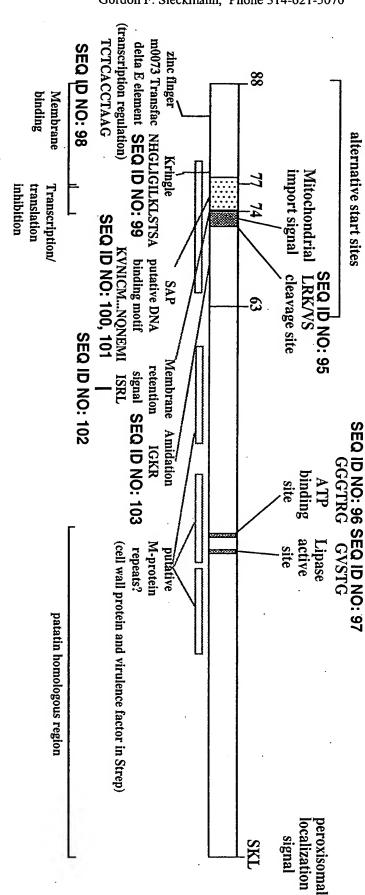
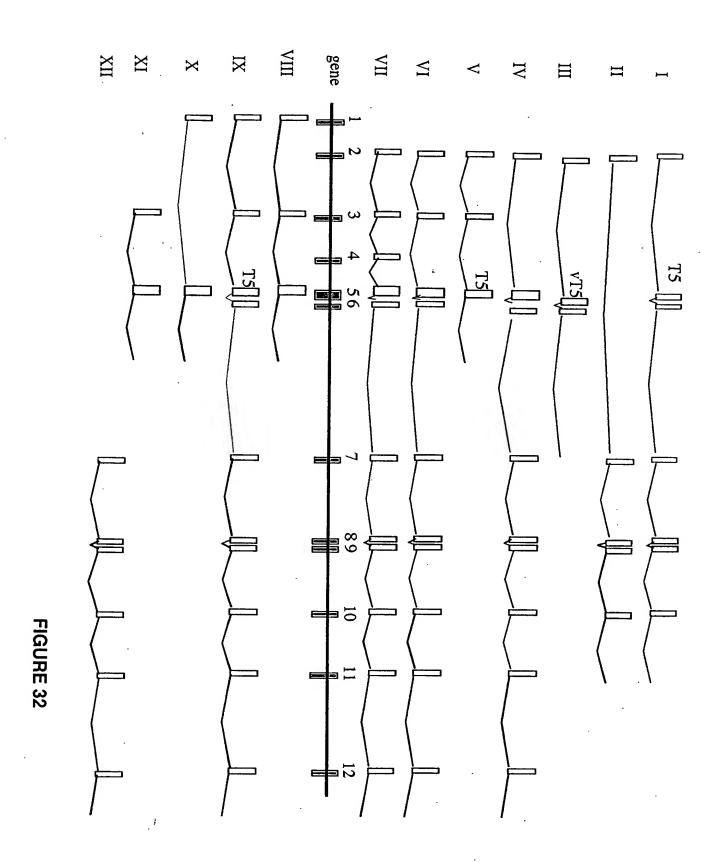


FIGURE 31

Inventor: Richard W. Gross et al. Docket No.: 15060-42

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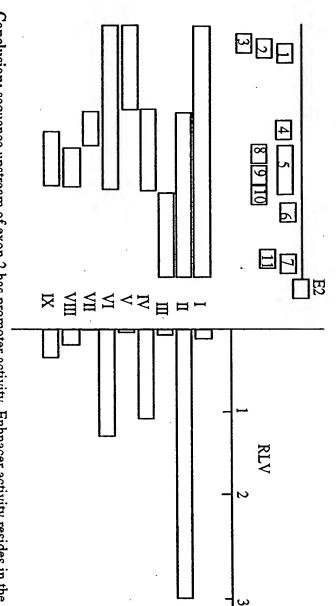


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44/61

FIGURE 33

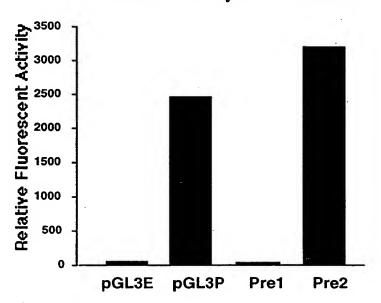
Promoter Analysis of iPLA27 Pre exon 2



are required for maximal inhibition. negative regulatory elements. Truncated fragments (II and VI) each lacking a GC region have enhanced promoter activity while GATA1 (9), p300 (4), and Gcr1 (10). GC regions upstream (1) and downstream (7) of this positive promoter region commonly are fragments (III and V) containing the GC regions but lacking region IV have minimal promoter activity. Presumably both GC regions (fragment IV). This region contains a CACG VNTR like seuqnece as well as sequences that match consensus sites for Sp1 (8), Conclusion: sequence upstream of exon 2 has promoter activity. Enhnacer activity resides in the region 200-400nt upstream of exon 2 mmediately upstream or downstream of region IV. Region IV may have less than optimal promoter activity if positive promtoer elements are

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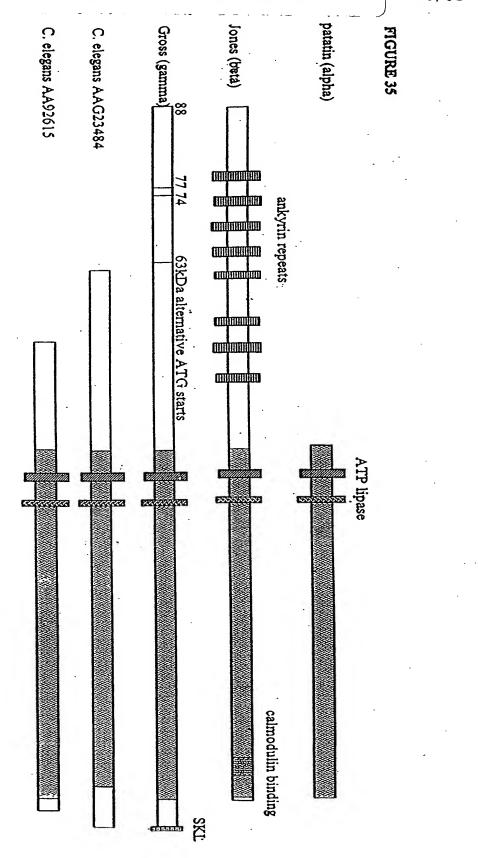
FIGURE 34. Promoter Activity of Pre Exon 1 and 2 Regions



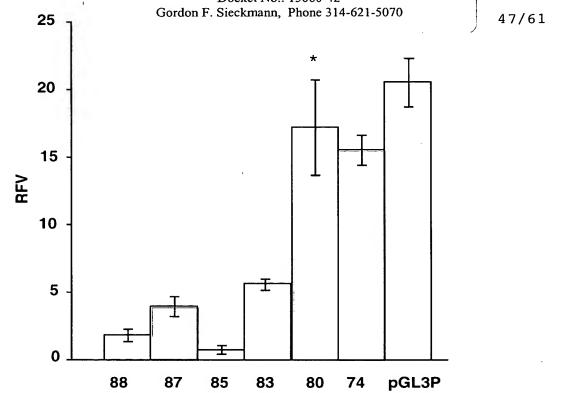
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Docket No.: 15060-42

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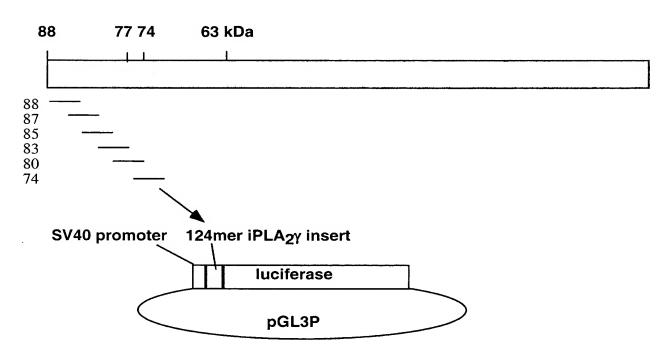


FIGURE 36

Inventor: Richard W. Gross et al.

Docket No.: 15060-42

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48/61

FIGURE 37



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Docket No.: 15060-42
Gordon F. Sieckmann, Phone 314-621-5070

49/61

1 2 3 4 5 6

-88kDa
-77kDa
-71kDa
-63kDa

FIGURE 38

Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

50/61

דוקטאנ

Mouse Rat Human

----AGGGTGAGG--CTG-TAGC---BCCAGTGTTTGBGGT

TGGGTGGTG--CTGGTCAC--

GCCAGTGTTTGGGGT

88

<u>=</u>

Alignment of Mouse, Rat, and Human Pre-exon 2 Sequence

SEQ ID NO

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51/61

FIGURE 40

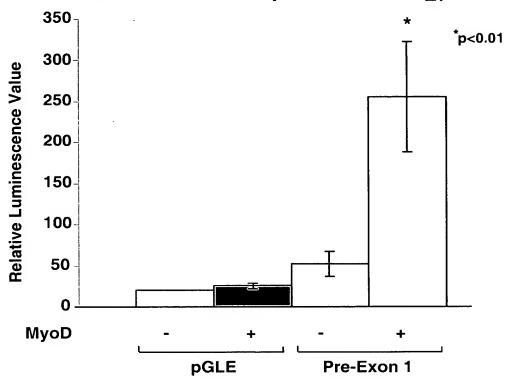


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52/61

MyoD Stimulation of Promoter Activity in Pre-Exon 1 Sequence of iPLA₂γ



Putative MyoD Elements within Pre-Exon 1 of iPLA27

-395	-336
ATTATAATACTGTGCAGCAAGGGCAATAAGAGAAGTGAGCA <u>C</u>	AGGTGGAAGGAATGATTC
GGA <u>C.</u>	<u>AGGTG</u> GG
E-box	(KX6D)
-335	-133
ATTCTATGAGTAGTGAGGTAAGATTTTCCTGGCTGAAGGACA	AACAAATCTTTAGGAGGA
-137	-99
-15, CAAGGTGGAAGGGGAGCTAAGCCAACAGCATGACCAAGGCAC	
-76	-17
AGAGTATCTGGGGAAGTACAGGTGTGGCTGGAGGATAGAGAG	TGAGAGGCAAGTGGTGAA
CACAGGTGGTG	CGACAGGTGGTG
E-box (MyoD)	E-рох (<u>%хо́р</u>)
-16 -1 1	

-16 -1 1
AGTAAAGGCTGGAAGG TCAGCAGGGTCAGA
Exem 1

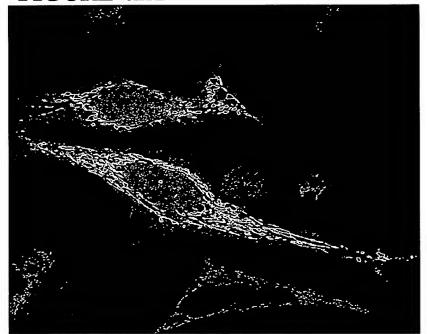
THEREFOR

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53/61

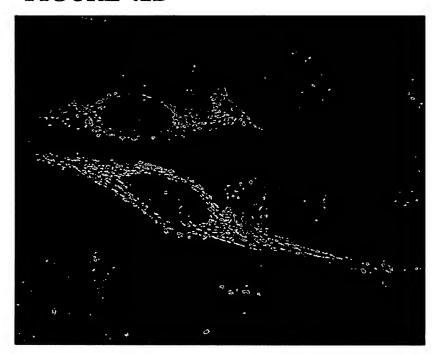
FIGURE 42A



Inventor: Richard W. Gross et al. Docket No.: 15060-42 Gordon F. Sieckmann, Phone 314-621-5070

54/61

FIGURE 42B

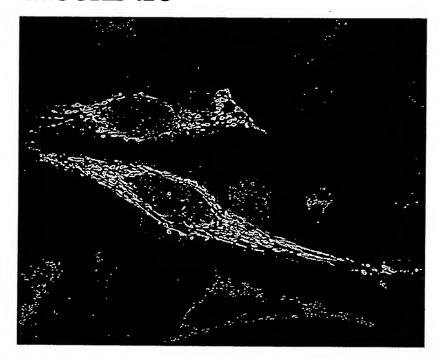


Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

55/61

FIGURE 42C



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Gordon F. Sieckmann, Phone 314-621-5070

					Table I
	Exon Number	Length (nt)	5' Intron Sequence	Corresponding AC005058 Residues	Sequence 3' Intron Sequence
	1 GTATGG	346	GGAAGG	135622-135327	SEQ ID NO: 29 TCAGCAGGGTCAGAACCTATAATTTCATTCGGTATATTCT
	-	-			GTGAAGATGTACAGCCAGCAAAAGCTTTTTAATTCGGGAA AACACGATTGGACTTGCACTTTCAAAAGATTACCGTGGTT GCACAGAAGACTGACTGACTGGGTCAGAGGTTAGTTACAGGC TGGAAAACCAGTTTAGATGAAACTGAAGAGCAAGGATGAA AGCCTGAACTAGAGCAGTGGAAATGCGAATGTGGAGCAGA GGAACGATTCAAGAAATTCTGCGGTAAAACTCATCAGACT TCATGACTGATTAAAG
-	4 GT AGGT	112	TCATAG	125571-125460	SEQ ID NO: 30 TITTGCCTTTCTAGAGTGTTATACAGCTGGAATCATACTG
			·		CTATGGTCCGAATGTTTGTGCCTCTCAAAATTCATGTGGA AATCATAACCGCTAAAGTGATGGTATTAAGAG

Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

		-	. •			.)	
VШ	VII	ZI	<	M	Ħ	п	Variant
e1/3/5	e2/3/4/5	e2/3/5	e2/3/t5	e2/5	e2/t5	e2/TT5BI562455 e2/T7 AI	Exons ESTs
AV747051; AV747330	BG723923	AA143503 BG502179 BG613307; BG701929; BG702929; BI547339 BG613307; BG719485; BG502179;BG771750 BG719485; BG613307	BG699526;BG699526; BI550880 AL529506 R64045	AF263947 BI596690; BI333453; BI553295 BG706376; BG708220 BG392963 AB041261	BI333454	2455 AL59775	Clone
	502	460.7	507	478 500	462		ne
pituitary	testis heart	colon embryonal carcinoma hippocampus testis	hippocampus neuroblastoma smooth muscle	heart hippocampus hypothalmus testis TlymphoJrkat smooth muscle	cervix heart	testis unknown	Source

Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

X ×	•	X	Variant
e1/t5 e3/5		e1/3/t5 AU136710; AK024335	Exons ESTs
466 460.1 pan ap2/466.5	494	492 467 485; 490	Table II (Continued) Clone
myocardial pancreas pancreatic	smooth muscle	placenta HUVEC pancreas smooth muscle	Source

Inventor: Richard W. Gross et al. Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

59/61

Construct	t Primer pairs	5' to 3' Sequence	SEO ID NO:
88	88f	GTTG <u>AAGCTT</u> GTGTCTATTAATCTGACTGTA	63
	788 188	TAGA <u>CCATGG</u> TGGCTTATCCTCCAGTAATGC	64
87	87f	GTGT <u>AAGCTT</u> GAAGCAGGAAGCAAGCAACTG	65
	87r	${\tt ACTG}{\underline{CCATGG}}{\tt TGGCCTTCACTTTTGGTCCATTTAC}$	66
85	85f	TGGA <u>AAGCTT</u> GCCACATCAGTCTACAAAG	67
	85r	TGCT <u>CCATGG</u> TGGCATCCCAATATGTAAACCA	88
83	83f	GAACCAAGCTTGAAGCACATTCTTGCAGTAAGCA	69
	83r	CAAAACATGTTGGCTACGGGACATACAAATGTTCA	70
80	80f	GTTG <u>AAGCTT</u> TTTGAAACTTAGCACTTCTGC	71
	·80r	ATT <u>CCATGG</u> TGGCTGAAATCATTTCATTTTGATTGCC	72
74	74f	TCAAAAGCTTATGATTTCACGTTTAGCTC	73
	741	CTTT <u>CCATGG</u> TGGCTGTCACTATATTTTTTCA	74

Table I

Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

III	Splice Variant
Юμ	S' Exon Number
GATTAAAG GCATCCCG	3' Exon Residues
	5' Intron Sequence
acctccttag	3' Intron Sequence
TAATGCAAG TAATGCAAG	5' Truncated Exon, SEQ ID NO. 5 Sequence
75,76 91,92	SEQ ID No:

Inventor: Richard W. Gross et al.

Docket No.: 15060-42

Gordon F. Sieckmann, Phone 314-621-5070

consensus	<u>NO:</u> 88kDa 77kDa 74kDa 63kDa	Isoform
G	D A O A	Se <u>S</u> eguence
C	PABH	Jue
C	T T A A G A G	Se
വ	C P P H	equ
GCCGCCACC <u>ATG</u> G	TTTTAAGTTATGTACTAAAAATGAAAAAAAAATGT	enc
O +	Внны	e s
G Þ	≯ G H ⊅	urr
C	२ २० ०	rno
C	ннкк	ndii
A	F K K K	ng n
H	HHHP	Table V ; iPLLA ₂
က	G G G H	le \ LA
'വ	,H,A,H,0	27
	'н	AT Ma
	1/12 adequ 1/12 poor 1/12 poor 1/12 poor 2/12 adequ	Table V Sequence surrounding iPLLA ₂ γ ATG Start Sites Matches to Koz
	1/12 adequate 1/12 poor 1/12 poor 1/12 poor 2/12 adequate	ATG Start Sites Matches to Kozak Consensus, SFO I
	7.5 8.8 8.2	7 10 1